SEQUENCE LISTING

<110>   Neose Technologies, Inc.
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        Hakes, David
        Chen, Xi
        Bowe, Caryne

<120>   GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
        METHODS

<130>   040853-01-5051WO

<150>   US 60/328,523
<151>   2001-10-10

<150>   US 60/334,233
<151>   2001-11-28

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<150>   US 10/360,770
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Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
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Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
    50                  55                  60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
65                  70                  75                  80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
                85                  90                  95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
            100                 105                 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
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Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
        35   40   45

Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
    50   55   60

Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
65   70   75   80

Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
                85   90   95

Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
            100   105   110

Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
        115   120   125

Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
    130   135   140

Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
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Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
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120

ctcctgtggc aattgaatgg gaggcttgaa tattgcctca aggacaggat gaactttgac
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atccctgagg agattaagca gctgcagcag ttccagaagg aggacgccgc attgaccatc
240

tatgagatgc tccagaacat ctttgctatt ttcagacaag attcatctag cactggctgg
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			20				25					30			

Ser	Ser	Asn	Phe	Gln	Cys	Gln	Lys	Leu	Leu	Trp	Gln	Leu	Asn	Gly	Arg
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Leu	Glu	Tyr	Cys	Leu	Lys	Asp	Arg	Met	Asn	Phe	Asp	Ile	Pro	Glu	Glu
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Tyr	His	Gln	Ile	Asn	His	Leu	Lys	Thr	Val	Leu	Glu	Glu	Lys	Leu	Glu
		115					120					125			

Lys	Glu	Asp	Phe	Thr	Arg	Gly	Lys	Leu	Met	Ser	Ser	Leu	His	Leu	Lys
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Arg	Tyr	Tyr	Gly	Arg	Ile	Leu	His	Tyr	Leu	Lys	Ala	Lys	Glu	Tyr	Ser
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Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
        35   40   45

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
    50   55   60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65   70   75   80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
                85   90   95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
            100   105   110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
        115   120   125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
    130   135   140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
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Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
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Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
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Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
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Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
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Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225   230   235   240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
                245   250   255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
            260   265   270

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
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Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
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Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
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Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
                325             330             335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
            340             345             350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
        355             360             365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
    370             375             380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385             390             395             400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
            405             410             415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
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Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn

                35   40   45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
    50   55   60

Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn
65   70   75   80

Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
                85   90   95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
            100   105   110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
        115   120   125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
    130   135   140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
145   150   155   160

Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
            165   170   175

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
            180   185   190

Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu
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Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe
    210   215   220

Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
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Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
            245   250   255

Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
        260   265   270

Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
    275   280   285

His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His
    290   295   300

Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu
305   310   315   320

Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys
            325   330   335

Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
            340   345   350

Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu
        355   360   365

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His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His
                405              410                  415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp
            420              425              430

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            20   25   30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
        35   40   45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
    50   ·55   60

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65   70   75   80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
                85   90   95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
            100   105   110

Tyr His Lys Ser
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<213> Homo sapiens

<400> 13
atgaagacac tccagttttt cttccttttc tgttgctgga aagcaatctg ctgcaatagc
60

tgtgagctga ccaacatcac cattgcaata gagaaagaag aatgtcgttt ctgcataagc
120

atcaacacca cttggtgtgc tggctactgc tacaccaggg atctggtgta taggaccca
180

gccaggccca aaatccagaa aacatgtacc ttcaaggaac tggtatatga aacagtgaga
240

gtgcccggct gtgctcacca tgcagattcc ttgtatacat acccagtggc cacccagtgt
300

cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct ggggcccagc
360

tactgctcct ttggtgaaat gaaagaataa
390

<210> 14
<211> 129
<212> PRT
<213> Homo sapiens

<400> 14
Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile

```
   1            5                  10              15
```

Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys
         20   25   30

Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly
         35   40   45

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
   50   55   60

Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg
65   70   75   80

Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val
             85   90   95

Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
         100   105   110

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys
         115   120   125

Glu

```
<210>  15
<211>  1342
<212>  DNA
<213>  Homo sapiens

<400>  15
cccggagccg gaccggggcc accgcgcccg ctctgctccg acaccgcgcc ccctggacag
60

ccgccctctc ctccaggccc gtggggctgg ccctgcaccg ccgagcttcc cgggatgagg
120

gcccccggtg tggtcacccg gcgcgcccca ggtcgctgag ggaccccggc caggcgcgga
180

gatgggggtg cacgaatgtc ctgcctggct gtggcttctc ctgtccctgc tgtcgctccc
240

tctgggcctc ccagtcctgg gcgccccacc acgcctcatc tgtgacagcc gagtcctgga
300

gaggtacctc ttggaggcca aggaggccga gaatatcacg acgggctgtg ctgaacactg
360

cagcttgaat gagaatatca ctgtcccaga caccaaagtt aatttctatg cctggaagag
420

gatggaggtc gggcagcagg ccgtagaagt ctggcagggc ctggccctgc tgtcggaagc
480

tgtcctgcgg ggccaggccc tgttggtcaa ctcttcccag ccgtgggagc ccctgcagct
540

gcatgtggat aaagccgtca gtggccttcg cagcctcacc actctgcttc gggctctgcg
600
```

agcccagaag gaagccatct cccctccaga tgcggcctca gctgctccac tccgaacaat
660

cactgctgac actttccgca aactcttccg agtctactcc aatttcctcc ggggaaagct
720

gaagctgtac acaggggagg cctgcaggac aggggacaga tgaccaggtg tgtccacctg
780

ggcatatcca ccacctccct caccaacatt gcttgtgcca caccctcccc cgccactcct
840

gaaccccgtc gaggggctct cagctcagcg ccagcctgtc ccatggacac tccagtgcca
900

gcaatgacat ctcaggggcc agaggaactg tccagagagc aactctgaga tctaaggatg
960

tcacagggcc aacttgaggg cccagagcag gaagcattca gagagcagct ttaaactcag
1020

ggacagagcc atgctgggaa gacgcctgag ctcactcggc accctgcaaa atttgatgcc
1080

aggacacgct ttggaggcga tttacctgtt ttcgcaccta ccatcaggga caggatgacc
1140

tggagaactt aggtggcaag ctgtgacttc tccaggtctc acgggcatgg gcactccctt
1200

ggtggcaaga gcccccttga caccggggtg gtgggaacca tgaagacagg atgggggctg
1260

gcctctggct ctcatggggt ccaagttttg tgtattcttc aacctcattg acaagaactg
1320

aaaccaccaa aaaaaaaaaa aa
1342

<210>   16
<211>   193
<212>   PRT
<213>   Homo sapiens

<400>   16
Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1   5   10   15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
            20   25   30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
            35   40   45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
        50   55   60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65   70   75   80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
                    85   90   95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
                100   105   110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
            115   120   125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
        130   135   140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145   150   155   160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
                165   170   175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
                180   185   190

Arg

<210>   17
<211>   435
<212>   DNA
<213>   Homo sapiens

<400>   17
atgtggctgc agagcctgct gctcttgggc actgtggcct gcagcatctc tgcacccgcc
60

cgctcgccca gccccagcac gcagccctgg gagcatgtga atgccatcca ggaggcccgg
120

cgtctcctga acctgagtag agacactgct gctgagatga atgaaacagt agaagtcatc
180

tcagaaatgt ttgacctcca ggagccgacc tgcctacaga cccgcctgga gctgtacaag
240

cagggcctgc ggggcagcct caccaagctc aagggcccct tgaccatgat ggccagccac
300

tacaagcagc actgccctcc aaccccggaa acttcctgtg caacccagat tatcaccttt
360

gaaagtttca aagagaacct gaaggacttt ctgcttgtca tcccctttga ctgctgggag
420

ccagtccagg agtga
435

<210>   18
<211>   144
<212>   PRT
<213>   Homo sapiens

<400>   18
Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile

```
 1             5                    10                    15
```

Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
            20   25   30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
            35   40   45

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
    50   55   60

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
65   70   75   80

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
                85   90   95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
            100   105   110

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
            115   120   125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
    130   135   140

<210>   19
<211>   501
<212>   DNA
<213>   Homo sapiens

<400>   19
atgaaatata caagttatat cttggctttt cagctctgca tcgttttggg ttctcttggc
60

tgttactgcc aggacccata tgtaaaagaa gcagaaaacc ttaagaaata ttttaatgca
120

ggtcattcag atgtagcgga taatggaact cttttcttag cattttgaa gaattggaaa
180

gaggagagtg acagaaaaat aatgcagagc caaattgtct ccttttactt caaacttttt
240

aaaaacttta agatgacca gagcatccaa agagtgtgg agaccatcaa ggaagacatg
300

aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat
360

tattcggtaa ctgacttgaa tgtccaacgc aaagcaatac atgaactcat ccaagtgatg
420

gctgaactgt cgccagcagc taaaacaggg aagcgaaaaa ggagtcagat gctgtttcga
480

ggtcgaagag catcccagta a
501

<210>   20
<211>   166
```

<212> PRT
<213> Homo sapiens

<400> 20
Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
1               5                   10                  15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
            20                  25                  30

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
        35                  40                  45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
    50                  55                  60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
65                  70                  75                  80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
                85                  90                  95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
            100                 105                 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
        115                 120                 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
    130                 135                 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
145                 150                 155                 160

Gly Arg Arg Ala Ser Gln
            165

<210> 21
<211> 1352
<212> DNA
<213> Homo sapiens

<400> 21
ctgggacagt gaatcgacaa tgccgtcttc tgtctcgtgg ggcatcctcc tgctggcagg
60

cctgtgctgc ctggtccctg tctccctggc tgaggatccc cagggagatg ctgcccagaa
120

gacagataca tcccaccatg atcaggatca cccaaccttc aacaagatca ccccaacct
180

ggctgagttc gccttcagcc tataccgcca gctggcacac cagtccaaca gcaccaatat
240

cttcttctcc ccagtgagca tcgctacagc ctttgcaatg ctctccctgg ggaccaaggc
300

tgacactcac gatgaaatcc tggagggcct gaatttcaac ctcacggaga ttccggaggc
360

tcagatccat gaaggcttcc aggaactcct ccgtaccctc aaccagccag acagccagct
420

ccagctgacc accggcaatg gcctgttcct cagcgagggc ctgaagctag tggataagtt
480

tttggaggat gttaaaaagt tgtaccactc agaagccttc actgtcaact cggggacac
540

cgaagaggcc aagaaacaga tcaacgatta cgtggagaag ggtactcaag ggaaaattgt
600

ggatttggtc aaggagcttg acagagacac agtttttgct ctggtgaatt acatcttctt
660

taaaggcaaa tgggagagac cctttgaagt caaggacacc gaggaagagg acttccacgt
720

ggaccaggtg accaccgtga aggtgcctat gatgaagcgt ttaggcatgt ttaacatcca
780

gcactgtaag aagctgtcca gctgggtgct gctgatgaaa tacctgggca atgccaccgc
840

catcttcttc ctgcctgatg aggggaaact acagcacctg gaaaatgaac tcacccacga
900

tatcatcacc aagttcctgg aaaatgaaga cagaaggtct gccagcttac atttacccaa
960

actgtccatt actggaacct atgatctgaa gagcgtcctg ggtcaactgg gcatcactaa
1020

ggtcttcagc aatggggctg acctctccgg ggtcacagag gaggcacccc tgaagctctc
1080

caaggccgtg cataaggctg tgctgaccat cgacgagaaa gggactgaag ctgctggggc
1140

catgttttta gaggccatac ccatgtctat cccccccgag gtcaagttca acaaaccctt
1200

tgtcttctta atgattgaac aaaataccaa gtctcccctc ttcatgggaa aagtggtgaa
1260

tcccacccaa aaataactgc ctctcgctcc tcaacccctc ccctccatcc ctggccccct
1320

ccctggatga cattaaagaa gggttgagct gg
1352


<210> 22
<211> 418
<212> PRT
<213> Homo sapiens

<400> 22
Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
1                5                    10                    15

Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala

Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
        35                  40                  45

Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
    50                  55                  60

Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
65                  70                  75                  80

Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
                85                  90                      95

His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
            100                 105                 110

Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
        115                 120                 125

Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
    130             .       135                 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
145                 150                 155                 160

Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
            165                 170                 175

Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
        180                 185                 190

Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
    195                 200                 205

Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
    210             215                 220

Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
225             230                 235                 240

Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
            245                 250                 255

Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
            260                 265                 270

Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
        275                 280                 285

Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
    290                 295                 300

Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
305             310                 315                 320

Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
                325                 330                 335

Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
            340                 345                 350

```
Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
        355             360             365
```

```
Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
    370             375             380
```

```
Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
385             390             395             400
```

```
Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
            405             410             415
```

Gln Lys

```
<210>   23
<211>   2004
<212>   DNA
<213>   Homo sapiens

<400>   23
gctaacctag tgcctatagc taaggcaggt acctgcatcc ttgtttttgt ttagtggatc
60

ctctatcctt cagagactct ggaacccctg tggtcttctc ttcatctaat gaccctgagg
120

ggatggagtt ttcaagtcct tccagagagg aatgtcccaa gcctttgagt agggtaagca
180

tcatggctgg cagcctcaca ggtttgcttc tacttcaggc agtgtcgtgg gcatcaggtg
240

cccgcccctg catccctaaa agcttcggct acagctcggt ggtgtgtgtc tgcaatgcca
300

catactgtga ctcctttgac cccccgacct ttcctgccct tggtaccttc agccgctatg
360

agagtacacg cagtgggcga cggatggagc tgagtatggg gcccatccag gctaatcaca
420

cgggcacagg cctgctactg accctgcagc cagaacagaa gttccagaaa gtgaagggat
480

ttggaggggc catgacagat gctgctgctc tcaacatcct tgccctgtca ccccctgccc
540

aaaatttgct acttaaatcg tacttctctg aagaaggaat cggatataac atcatccggg
600

tacccatggc cagctgtgac ttctccatcc gcacctacac ctatgcagac acccctgatg
660

atttccagtt gcacaacttc agcctcccag aggaagatac caagctcaag ataccccctga
720

ttcaccgagc cctgcagttg gcccagcgtc ccgtttcact ccttgccagc ccctggacat
780
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cacccacttg gctcaagacc aatggagcgg tgaatgggaa ggggtcactc aagggacagc
840

ccggagacat ctaccaccag acctgggcca gatactttgt gaagttcctg gatgcctatg
900

ctgagcacaa gttacagttc tgggcagtga cagctgaaaa tgagccttct gctgggctgt
960

tgagtggata ccccttccag tgcctgggct tcacccctga acatcagcga gacttcattg
1020

cccgtgacct aggtcctacc ctcgccaaca gtactcacca caatgtccgc ctactcatgc
1080

tggatgacca acgcttgctg ctgccccact gggcaaaggt ggtactgaca gacccagaag
1140

cagctaaata tgttcatggc attgctgtac attggtacct ggactttctg gctccagcca
1200

aagccaccct aggggagaca caccgcctgt ccccaacac catgctcttt gcctcagagg
1260

cctgtgtggg ctccaagttc tgggagcaga gtgtgcggct aggctcctgg gatcgaggga
1320

tgcagtacag ccacagcatc atcacgaacc tcctgtacca tgtggtcggc tggaccgact
1380

ggaaccttgc cctgaacccc gaaggaggac ccaattgggt gcgtaacttt gtcgacagtc
1440

ccatcattgt agacatcacc aaggacacgt tttacaaaca gcccatgttc taccaccttg
1500

gccacttcag caagttcatt cctgagggct cccagagagt ggggctggtt gccagtcaga
1560

agaacgacct ggacgcagtg gcactgatgc atcccgatgg ctctgctgtt gtggtcgtgc
1620

taaaccgctc ctctaaggat gtgcctctta ccatcaagga tcctgctgtg ggcttcctgg
1680

agacaatctc acctggctac tccattcaca cctacctgtg catcgccag tgatggagca
1740

gatactcaag gaggcactgg gctcagcctg ggcattaaag ggacagagtc agctcacacg
1800

ctgtctgtga ctaaagaggg cacagcaggg ccagtgtgag cttacagcga cgtaagccca
1860

ggggcaatgg tttgggtgac tcactttccc ctctaggtgg tgcccagggc tggaggcccc
1920

tagaaaaaga tcagtaagcc ccagtgtccc cccagccccc atgcttatgt gaacatgcgc
1980
```

tgtgtgctgc ttgctttgga aact
2004

```
<210>    24
<211>    536
<212>    PRT
<213>    Homo sapiens

<400>    24
Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser
1                 5                  10                 15

Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
            20                  25                  30

Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
        35                  40                  45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
    50                  55                  60

Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
65                  70                  75                  80

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
            85                  90                  95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
            100                 105                 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
    115                 120                 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
    130                 135                 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
145                 150                 155                 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
            165                 170                 175

Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
            180                 185                 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
    195                 200                 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
    210                 215                 220

Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
225                 230                 235                 240

Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
            245                 250                 255

Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
            260                 265                 270

Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
```

Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
    290   295   300

Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
305   310   315   320

Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
            325   330   335

Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
        340   345   350

Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
        355   360   365

Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
    370   375   380

Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
385   390   395   400

Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
            405   410   415

Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
            420   425   430

Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
        435   440   445

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
    450   455   460

Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
465   470   475   480

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
            485   490   495

Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
        500   505   510

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
        515   520   525

His Thr Tyr Leu Trp His Arg Gln
    530   535

<210> 25
<211> 1726
<212> DNA
<213> Homo sapiens

<400> 25
atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt
60

tcgcccagcc aggaaatcca tgcccgattc agaagaggag ccagatctta ccaagtgatc
120

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tgcagagatg aaaaaacgca gatgatatac cagcaacatc agtcatggct gcgccctgtg
180

ctcagaagca accgggtgga atattgctgg tgcaacagtg cagggcaca gtgccactca
240

gtgcctgtca aaagttgcag cgagccaagg tgtttcaacg ggggcacctg ccagcaggcc
300

ctgtacttct cagatttcgt gtgccagtgc cccgaaggat ttgctgggaa gtgctgtgaa
360

atagatacca gggccacgtg ctacgaggac cagggcatca gctacagggg cacgtggagc
420

acagcggaga gtggcgccga gtgcaccaac tggaacagca cgcgttggc ccagaagccc
480

tacagcgggc ggaggccaga cgccatcagg ctgggcctgg ggaaccacaa ctactgcaga
540

aacccagatc gagactcaaa gccctggtgc tacgtcttta aggcggggaa gtacagctca
600

gagttctgca gcacccctgc ctgctctgag ggaaacagtg actgctactt tgggaatggg
660

tcagcctacc gtggcacgca cagcctcacc gagtcgggtg cctcctgcct cccgtggaat
720

tccatgatcc tgataggcaa ggtttacaca gcacagaacc ccagtgccca ggcactgggc
780

ctgggcaaac ataattactg ccggaatcct gatggggatg ccaagccctg gtgccacgtg
840

ctgaagaacc gcaggctgac gtgggagtac tgtgatgtgc cctcctgctc cacctgcggc
900

ctgagacagt acagccagcc tcagtttcgc atcaaaggag gctcttcgc cgacatcgcc
960

tcccacccct ggcaggctgc catctttgcc aagcacagga ggtcgccggg agagcggttc
1020

ctgtgcgggg gcatactcat cagctcctgc tggattctct ctgccgccca ctgcttccag
1080

gagaggtttc cgccccacca cctgacggtg atcttgggca gaacataccg ggtggtccct
1140

ggcgaggagg agcagaaatt tgaagtcgaa aaatacattg tccataagga attcgatgat
1200

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1260

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Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
            35   40   45

Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
    50   55   60

Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
65   70   75   80

Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
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Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
            100   105   110

Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
        115   120   125

Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
    130   135   140

Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
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Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
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Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
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Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
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Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
225   230   235   240

Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala
       245   250   255

Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly
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Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp
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Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr
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Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala
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Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro
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Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile
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Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu
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Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu
   370   375   380

Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp
385   390   395   400

Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser
     405   410   415

Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro
    420   425   430

Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly
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Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
   450   455   460

Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His
465   470   475   480

Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr
    485   490   495

Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp
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Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val
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Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu
        35   40   45

Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr
    50   55   60

Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys Gln Leu Gln
65   70   75   80

Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala
                85   90   95

Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile
            100   105   110

Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys
        115   120   125

Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp
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Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
            35                  40                  45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
    50                  55                  60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65                  70                  75                  80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
                85                  90                  95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
            100                 105                 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
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Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
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Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
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Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
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Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
            260   265   270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
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Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
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Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
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            435   440   445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
    450   455   460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
465   470   475   480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
            485   490   495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
            500   505   510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
            515   520   525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
    530   535   540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
545   550   555   560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
            565   570   575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
            580   585   590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
        595   600   605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
    610   615   620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
625   630   635   640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
            645   650   655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
            660   665   670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
            675   680   685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
    690   695   700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
705   710   715   720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
            725   730   735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
            740   745   750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg
            755   760   765

Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp
    770   775   780

Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys
785   790   795   800

Ile Gln Asn Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser
            805   810   815

Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr
            820   825   830

Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
            835   840   845

Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly
850   855   860

Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
865   870   875   880

Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
                885   890   895

Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
            900   905   910

Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met
        915   920   925

Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
    930   935   940

Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu
945   950   955   960

Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu
            965   970   975

Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
        980   985   990

Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala
    995   1000   1005

Leu Phe Lys Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser
    1010   1015   1020

Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser
    1025   1030   1035

Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu
    1040   1045   1050

Ser Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg
    1055   1060   1065

Met Leu Met Asp Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met
    1070   1075   1080

Ser Asn Lys Thr Thr Ser Ser Lys Asn Met Glu Met Val Gln Gln
    1085   1090   1095

Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala Gln Asn Pro Asp Met
    1100   1105   1110

Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg Trp Ile
    1115   1120   1125

Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro
    1130   1135   1140

Ser Pro Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu
    1145   1150   1155

Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys Val Val Val Gly Lys

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       1160                      1165                     1170
Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu Met Val Phe Pro
    1175                 1180                 1185

Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn Leu His Glu
    1190                 1195                 1200

Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile Glu
    1205                 1210                 1215

Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile
    1220                 1225                 1230

His Thr Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu
    1235                 1240                 1245

Leu Ser Thr Arg Gln Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr
    1250                 1255                 1260

Ala Pro Val Leu Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn
    1265                 1270                 1275

Arg Thr Lys Lys His Thr Ala His Phe Ser Lys Lys Gly Glu Glu
    1280                 1285                 1290

Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val Glu
    1295                 1300                 1305

Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln
    1310                 1315                 1320

Asn Phe Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg
    1325                 1330                 1335

Leu Pro Leu Glu Glu Thr Glu Leu Glu Lys Arg Ile Ile Val Asp
    1340                 1345                 1350

Asp Thr Ser Thr Gln Trp Ser Lys Asn Met Lys His Leu Thr Pro
    1355                 1360                 1365

Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu Lys Gly Ala
    1370                 1375                 1380

Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser
    1385                 1390                 1395

Ile Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser
    1400                 1405                 1410

Ser Phe Pro Ser Ile Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe
    1415                 1420                 1425

Gln Asp Asn Ser Ser His Leu Pro Ala Ala Ser Tyr Arg Lys Lys
    1430                 1435                 1440

Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly Ala Lys
    1445                 1450                 1455

Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr Gly
    1460                 1465                 1470
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Asp Gln  Arg Glu Val Gly Ser  Leu Gly Thr Ser Ala  Thr Asn Ser
    1475              1480              1485

Val Thr  Tyr Lys Lys Val Glu  Asn Thr Val Leu Pro  Lys Pro Asp
    1490              1495              1500

Leu Pro  Lys Thr Ser Gly Lys  Val Glu Leu Leu Pro  Lys Val His
    1505              1510              1515

Ile Tyr  Gln Lys Asp Leu Phe  Pro Thr Glu Thr Ser  Asn Gly Ser
    1520              1525              1530

Pro Gly  His Leu Asp Leu Val  Glu Gly Ser Leu Leu  Gln Gly Thr
    1535              1540              1545

Glu Gly  Ala Ile Lys Trp Asn  Glu Ala Asn Arg Pro  Gly Lys Val
    1550              1555              1560

Pro Phe  Leu Arg Val Ala Thr  Glu Ser Ser Ala Lys  Thr Pro Ser
    1565              1570              1575

Lys Leu  Leu Asp Pro Leu Ala  Trp Asp Asn His Tyr  Gly Thr Gln
    1580              1585              1590

Ile Pro  Lys Glu Glu Trp Lys  Ser Gln Glu Lys Ser  Pro Glu Lys
    1595              1600              1605

Thr Ala  Phe Lys Lys Lys Asp  Thr Ile Leu Ser Leu  Asn Ala Cys
    1610              1615              1620

Glu Ser  Asn His Ala Ile Ala  Ala Ile Asn Glu Gly  Gln Asn Lys
    1625              1630              1635

Pro Glu  Ile Glu Val Thr Trp  Ala Lys Gln Gly Arg  Thr Glu Arg
    1640              1645              1650

Leu Cys  Ser Gln Asn Pro Pro  Val Leu Lys Arg His  Gln Arg Glu
    1655              1660              1665

Ile Thr  Arg Thr Thr Leu Gln  Ser Asp Gln Glu Glu  Ile Asp Tyr
    1670              1675              1680

Asp Asp  Thr Ile Ser Val Glu  Met Lys Lys Glu Asp  Phe Asp Ile
    1685              1690              1695

Tyr Asp  Glu Asp Glu Asn Gln  Ser Pro Arg Ser Phe  Gln Lys Lys
    1700              1705              1710

Thr Arg  His Tyr Phe Ile Ala  Ala Val Glu Arg Leu  Trp Asp Tyr
    1715              1720              1725

Gly Met  Ser Ser Ser Pro His  Val Leu Arg Asn Arg  Ala Gln Ser
    1730              1735              1740

Gly Ser  Val Pro Gln Phe Lys  Lys Val Val Phe Gln  Glu Phe Thr
    1745              1750              1755

Asp Gly  Ser Phe Thr Gln Pro  Leu Tyr Arg Gly Glu  Leu Asn Glu
    1760              1765              1770
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His Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp
    1775   1780   1785

Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser
    1790   1795   1800

Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly
    1805   1810   1815

Ala Glu Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr
    1820   1825   1830

Tyr Phe Trp Lys Val Gln His Met Ala Pro Thr Lys Asp Glu
    1835   1840   1845

Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu
    1850   1855   1860

Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His
    1865   1870   1875

Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln
    1880   1885   1890

Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp
    1895   1900   1905

Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn
    1910   1915   1920

Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His
    1925   1930   1935

Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met
    1940   1945   1950

Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser
    1955   1960   1965

Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr
    1970   1975   1980

Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr
    1985   1990   1995

Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly
    2000   2005   2010

Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly
    2015   2020   2025

Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro
    2030   2035   2040

Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala
    2045   2050   2055

Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His
    2060   2065   2070

Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser

```
            2075                  2080                    2085
Trp Ile  Lys Val Asp Leu Leu  Ala Pro Met Ile Ile  His Gly Ile
    2090                 2095                2100

Lys Thr  Gln Gly Ala Arg Gln  Lys Phe Ser Ser Leu  Tyr Ile Ser
    2105                 2110                2115

Gln Phe  Ile Ile Met Tyr Ser  Leu Asp Gly Lys Lys  Trp Gln Thr
    2120                 2125                2130

Tyr Arg  Gly Asn Ser Thr Gly  Thr Leu Met Val Phe  Phe Gly Asn
    2135                 2140                2145

Val Asp  Ser Ser Gly Ile Lys  His Asn Ile Phe Asn  Pro Pro Ile
    2150                 2155                2160

Ile Ala  Arg Tyr Ile Arg Leu  His Pro Thr His Tyr  Ser Ile Arg
    2165                 2170                2175

Ser Thr  Leu Arg Met Glu Leu  Met Gly Cys Asp Leu  Asn Ser Cys
    2180                 2185                2190

Ser Met  Pro Leu Gly Met Glu  Ser Lys Ala Ile Ser  Asp Ala Gln
    2195                 2200                2205

Ile Thr  Ala Ser Ser Tyr Phe  Thr Asn Met Phe Ala  Thr Trp Ser
    2210                 2215                2220

Pro Ser  Lys Ala Arg Leu His  Leu Gln Gly Arg Ser  Asn Ala Trp
    2225                 2230                2235

Arg Pro  Gln Val Asn Asn Pro  Lys Glu Trp Leu Gln  Val Asp Phe
    2240                 2245                2250

Gln Lys  Thr Met Lys Val Thr  Gly Val Thr Thr Gln  Gly Val Lys
    2255                 2260                2265

Ser Leu  Leu Thr Ser Met Tyr  Val Lys Glu Phe Leu  Ile Ser Ser
    2270                 2275                2280

Ser Gln  Asp Gly His Gln Trp  Thr Leu Phe Phe Gln  Asn Gly Lys
    2285                 2290                2295

Val Lys  Val Phe Gln Gly Asn  Gln Asp Ser Phe Thr  Pro Val Val
    2300                 2305                2310

Asn Ser  Leu Asp Pro Pro Leu  Leu Thr Arg Tyr Leu  Arg Ile His
    2315                 2320                2325

Pro Gln  Ser Trp Val His Gln  Ile Ala Leu Arg Met  Glu Val Leu
    2330                 2335                2340

Gly Cys  Glu Ala Gln Asp Leu  Tyr
    2345                 2350
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<210> 31
<211> 1471
<212> DNA
<213> Homo sapiens

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120

cggctcagag aatactatga ccagacagct cagatgtgct gcagcaaatg ctcgccgggc
180

caacatgcaa aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac
240

agcacataca cccagctctg gaactgggtt cccgagtgct tgagctgtgg ctcccgctgt
300

agctctgacc aggtggaaac tcaagcctgc actcgggaac agaaccgcat ctgcacctgc
360

aggcccggct ggtactgcgc gctgagcaag caggaggggt gccggctgtg cgcgccgctg
420

cgcaagtgcc gcccgggctt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg
480

tgcaagccct gtgccccggg gacgttctcc aacacgactt catccacgga tatttgcagg
540

ccccaccaga tctgtaacgt ggtggccatc cctgggaatg caagcatgga tgcagtctgc
600

acgtccacgt cccccacccg gagtatggcc caggggcag tacacttacc ccagccagtg
660

tccacacgat cccaacacac gcagccaact ccagaaccca gcactgctcc aagcacctcc
720

ttcctgctcc caatgggccc cagcccccca gctgaaggga gcactggcga cttcgctctt
780

ccagttggac tgattgtggg tgtgacagcc ttgggtctac taataatagg agtggtgaac
840

tgtgtcatca tgacccaggt gaaaaagaag cccttgtgcc tgcagagaga agccaaggtg
900

cctcacttgc ctgccgataa ggcccggggt acacagggcc ccgagcagca gcacctgctg
960

atcacagcgc cgagctccag cagcagctcc ctggagagct cggccagtgc gttggacaga
1020

agggcgccca ctcggaacca gccacaggca ccaggcgtgg aggccagtgg ggccggggag
1080

gcccgggcca gcaccgggag ctcagattct tcccctggtg ccatgggac ccaggtcaat
1140

gtcacctgca tcgtgaacgt ctgtagcagc tctgaccaca gctcacagtg ctcctcccaa
1200
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44

gccagctcca caatgggaga cacagattcc agcccctcgg agtccccgaa ggacgagcag
1260

gtccccttct ccaaggagga atgtgccttt cggtcacagc tggagacgcc agagaccctg
1320

ctggggagca ccgaagagaa gcccctgccc cttggagtgc ctgatgctgg gatgaagccc
1380

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1440

accctgcgaa ggggccctgg tccttccagg c
1471

<210> 32
<211> 461
<212> PRT
<213> Homo sapiens

<400> 32
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1   5   10   15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
            20   25   30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
        35   40   45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
    50   55   60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65   70   75   80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
                85   90   95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
            100   105   110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
            115   120   125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
        130   135   140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145   150   155   160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
                165   170   175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
            180   185   190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
        195   200   205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser

<pre>
         210   215   220

Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225   230   235   240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
                245   250   255

Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
            260   265   270

Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
        275   280   285

Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
    290   295   300

Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
305   310   315   320

Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
                325   330   335

Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
            340   345   350

Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
        355   360   365

Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
    370   375   380

Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
385   390   395   400

Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
                405   410   415

Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
            420   425   430

Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
        435   440   445

Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
    450   455   460
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<210> 33
<211> 1475
<212> DNA
<213> Homo sapiens

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120

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180

taaatggagg aacatgtgtg tccaacaagt acttctccaa cattcactgg tgcaactgcc
240

caaagaaatt cggagggcag cactgtgaaa tagataagtc aaaaacctgc tatgagggga
300

atggtcactt ttaccgagga aaggccagca ctgacaccat gggccggccc tgcctgccct
360

ggaactctgc cactgtcctt cagcaaacgt accatgccca cagatctgat gctcttcagc
420

tgggcctggg gaaacataat tactgcagga acccagacaa ccggaggcga ccctggtgct
480

atgtgcaggt gggcctaaag ccgcttgtcc aagagtgcat ggtgcatgac tgcgcagatg
540

gaaaaaagcc ctcctctcct ccagaagaat aaaatttca gtgtggccaa aagactctga
600

ggccccgctt taagattatt gggggagaat tcaccaccat cgagaaccag ccctggtttg
660

cggccatcta caggaggcac cgggggggct ctgtcaccta cgtgtgtgga ggcagcctca
720

tcagcccttg ctgggtgatc agcgccacac actgcttcat tgattaccca aagaaggagg
780

actacatcgt ctacctgggt cgctcaaggc ttaactccaa cacgcaaggg gagatgaagt
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ttgaggtgga aaacctcatc ctacacaagg actacagcgc tgacacgctt gctcaccaca
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acgacattgc cttgctgaag atccgttcca aggagggcag gtgtgcgcag ccatcccgga
960

ctatacagac catctgcctg ccctcgatgt ataacgatcc ccagtttggc acaagctgtg
1020

agatcactgg ctttggaaaa gagaattcta ccgactatct ctatccggag cagctgaaga
1080

tgactgttgt gaagctgatt tcccaccggg agtgtcagca gccccactac tacggctctg
1140

aagtcaccac caaaatgctg tgtgctgctg acccacagtg gaaaacagat tcctgccagg
1200

gagactcagg gggacccctc gtctgttccc tccaaggccg catgactttg actggaattg
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tgagctgggg ccgtggatgt gccctgaagg acaagccagg cgtctacacg agagtctcac
1320

acttcttacc ctggatccgc agtcacacca aggaagagaa tggcctggcc ctctgagggt
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1475

<210> 34
<211> 431
<212> PRT
<213> Homo sapiens

<400> 34
Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1   5   10   15

Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
            20   25   30

Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
        35   40   45

His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
    50   55   60

Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65   70   75   80

Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
                85   90   95

Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
            100   105   110

Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
        115   120   125

Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
    130   135   140

Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
145   150   155   160

Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
                165   170   175

Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
            180   185   190

Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
        195   200   205

Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
    210   215   220

Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
225   230   235   240

Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
                245   250   255

Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His

48

          260   265   270

His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
        275   280   285

Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
    290   295   300

Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
305   310   315   320

Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val
                325   330   335

Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly
            340   345   350

Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys
        355   360   365

Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu
    370   375   380

Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
385   390   395   400

Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
                405   410   415

Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
            420   425   430

<210>   35
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<212>   PRT
<213>   Mus musculus

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
            20   25   30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

<210>   36
<211>   120

<212> PRT
<213> Mus musculus

<400> 36
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
            20   25   30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
            85   90   95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 37
<211> 120
<212> PRT
<213> Mus musculus

<400> 37
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1   5   10   15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
            20   25   30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu
        35   40   45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
    50   55   60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65   70   75   80

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
            85   90   95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
            100   105   110

Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 38
<211> 106
<212> PRT

<210> Mus musculus

<400> 38

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	

Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Cys	Gln	Leu	Ser	Val	Gly	Tyr	Met
			20					25					30		

His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Trp	Ile	Tyr
		35					40					45			

Asp	Thr	Ser	Lys	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
	50					55					60				

Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Asp
65					70					75					80

Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	Gly	Tyr	Pro	Phe	Thr
			85					90					95		

Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105	

<210> 39
<211> 1039
<212> DNA
<213> Homo sapiens

<400> 39

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120

cattctcgtc atctctgagg acatcaccat catctcagga tgagggggcat gaagctgctg
180

ggggcgctgc tggcactggc ggccctactg caggggggccg tgtccctgaa gatcgcagcc
240

ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt
300

gtgcagatcc tgagccgcta tgacatcgcc ctggtccagg aggtcagaga cagccacctg
360

actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac
420

gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg
480

cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg
540

aacgacacct caaccgaga gccagccatt gtcaggttct ctcccggtt cacagaggtc
600
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agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac
660

gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttggagga cgtcatgttg
720

atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc
780

ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca
840

cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgccgtt
900

gttcccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg
960

gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc
1020

cacaccagtt gaactgcag
1039

<210>   40
<211>   282
<212>   PRT
<213>   Homo sapiens

<400>   40
Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu
1   5   10   15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
            20   25   30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
        35   40   45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
    50   55   60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
65   70   75   80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
                85   90   95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
            100   105   110

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
            115   120   125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
        130   135   140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
145   150   155   160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val

52

			165				170				175		

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
                180   185   190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
            195   200   205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
    210   215   220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
225   230   235   240

Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn
            245   250   255

Phe Gln Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser
        260   265   270

Asp His Tyr Pro Val Glu Val Met Leu Lys
        275   280

<210> 41
<211> 678
<212> DNA
<213> Mus musculus

<400> 41
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120

aatggttctc caaggcttct cataaagtat gcttctgagt ctatgtctgg gatcccttcc
180

aggtttagtg gcagtggatc agggacagat tttactctta gcatcaacac tgtggagtct
240

gaagatattg cagattatta ctgtcaacaa agtcatagct ggccattcac gttcggctcg
300

gggacaaatt tggaagtaaa agaagtgaag cttgaggagt ctggaggagg cttggtgcaa
360

cctggaggat ccatgaaact ctcctgtgtt gcctctggat tcattttcag taaccactgg
420

atgaactggg tccgccagtc tccagagaag gggcttgagt gggttgctga aattagatca
480

aaatctatta attctgcaac acattatgcg gagtctgtga aagggaggtt caccatctca
540

agagatgatt ccaaaagtgc tgtctacctg caaatgaccg acttaagaac tgaagacact
600

ggcgtttatt actgttccag gaattactac ggtagtacct acgactactg gggccaaggc
660

53

accactctca cagtctcc
678

<210>   42
<211>   226
<212>   PRT
<213>   Mus musculus

<400>   42
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
1   5   10   15

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
            20   25   30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
        35   40   45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
65   70   75   80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
                85   90   95

Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu
            100   105   110

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser
            115   120   125

Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val
    130   135   140

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser
145   150   155   160

Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg
                165   170   175

Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met
            180   185   190

Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn
        195   200   205

Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
    210   215   220

Val Ser
225

<210>   43
<211>   450
<212>   DNA
<213>   Homo sapiens

<400>   43

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60

gcctcctgcc cctgctggcg ctgctggccc tctggggacc tgacccagcc gcagcctttg
120

tgaaccaaca cctgtgcggc tcacacctgg tggaagctct ctacctagtg tgcggggaac
180

gaggcttctt ctacacaccc aagacccgcc gggaggcaga ggacctgcag gtggggcagg
240

tggagctggg cgggggccct ggtgcaggca gcctgcagcc cttggccctg gagggtccc
300

tgcagaagcg tggcattgtg aacaatgct gtaccagcat ctgctccctc taccagctgg
360

agaactactg caactagacg cagcccgcag gcagcccccc acccgccgcc tcctgcaccg
420

agagagatgg aataaagccc ttgaaccagc
450

<210>   44
<211>   110
<212>   PRT
<213>   Homo sapiens

<400>   44
Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1   5   10   15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
            20   25   30

Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
        35   40   45

Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
    50   55   60

Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
65   70   75   80

Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
                85   90   95

Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
                100   105   110

<210>   45
<211>   1203
<212>   DNA
<213>   Hepatitis B virus

<400>   45
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60

cctctgggat tctttcccga tcaccagttg gaccctgcgt tcggagccaa ctcaaacaat
120

ccagattggg acttcaaccc caacaaggat cactggccag aggcaatcaa ggtaggagcg
180

ggagacttcg ggccagggtt cacccCacca cacggcggtc ttttggggtg gagccctcag
240

gctcagggca tattgacaac agtgccagca gcgcctcctc ctgtttccac caatcggcag
300

tcaggaagac agcctactcc catctctcca cctctaagag acagtcatcc tcaggccatg
360

cagtggaact ccacaacatt ccaccaagct ctgctagatc ccagagtgag gggcctatat
420

tttcctgctg gtggctccag ttccggaaca gtaaaccctg ttccgactac tgtctcaccc
480

atatcgtcaa tcttctcgag gactggggac cctgcaccga acatggagag cacaacatca
540

ggattcctag gacccctgct cgtgttacag gcggggtttt tcttgttgac aagaatcctc
600

acaataccac agagtctaga ctcgtggtgg acttctctca attttctagg gggagcaccc
660

acgtgtcctg gccaaaattc gcagtcccca acctccaatc actcaccaac ctcttgtcct
720

ccaatttgtc ctggttatcg ctggatgtgt ctgcggcgtt ttatcatatt cctcttcatc
780

ctgctgctat gcctcatctt cttgttggtt cttctggact accaaggtat gttgcccgtt
840

tgtcctctac ttccaggaac atcaactacc agcacgggac catgcaagac ctgcacgatt
900

cctgctcaag gaacctctat gtttccctct tgttgctgta caaaaccttc ggacggaaac
960

tgcacttgta ttcccatccc atcatCctgg gctttcgcaa gattcctatg ggagtgggcc
1020

tcagtccgtt tctcctggct cagtttacta gtgccatttg ttcagtggtt cgcagggctt
1080

tcccccactg tttggctttc agttatatgg atgatgtggt attggggggcc aagtctgtac
1140

aacatcttga gtccctttttt acctctatta ccaattttct tttgtctttg ggtatacatt
1200

tga
1203

<210> 46

<211> 400
<212> PRT
<213> Hepatitis B virus

<400> 46
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Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
1               5                   10                  15

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
            20                  25                  30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
        35                  40                  45

Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly
    50                  55                  60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
65                  70                  75                  80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser
                85                  90                  95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
            100                 105                 110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
        115                 120                 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
    130                 135                 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro
145                 150                 155                 160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
                165                 170                 175

Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
            180                 185                 190

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
        195                 200                 205

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
    210                 215                 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
225                 230                 235                 240

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
                245                 250                 255

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
            260                 265                 270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
        275                 280                 285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
    290                 295                 300
```

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Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
305                 310             315                 320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
            325             330                 335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
            340             345             350

Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val
        355             360             365

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
    370             375             380

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
385             390             395                 400
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<210> 47
<211> 799
<212> DNA
<213> Homo sapiens

<400> 47
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120

cccaaccatt cccttatcca ggccttttga caacgctatg ctccgcgccc atcgtctgca
180

ccagctggcc tttgacacct accaggagtt tgaagaagcc tatatcccaa aggaacagaa
240

gtattcattc ctgcagaacc cccagacctc cctctgtttc tcagagtcta ttccgacacc
300

ctccaacagg gaggaaacac aacagaaatc aacctagag ctgctccgca tctccctgct
360

gctcatccag tcgtggctgg agcccgtgca gttcctcagg agtgtcttcg ccaacagcct
420          o

ggtgtacggc gcctctgaca gcaacgtcta tgacctccta aaggacctag aggaaggcat
480

ccaaacgctg atggggaggc tggaagatgg cagcccccgg actgggcaga tcttcaagca
540

gacctacagc aagttcgaca caaactcaca acgatgac gcactactca gaactacgg
600

gctgctctac tgcttcagga aggacatgga caaggtcgag acattcctgc gcatcgtgca
660

gtgccgctct gtggagggca gctgtggctt ctagctgccc gggtggcatc cctgtgaccc
720
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ctccccagtg cctctcctgg ccctggaagt tgccactcca gtgcccacca gccttgtcct
780

aataaaatta agttgcatc
799

<210> 48
<211> 217
<212> PRT
<213> Homo sapiens

<400> 48
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1   5   10   15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
                20   25   30

Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
            35   40   45

Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
        50   55   60

Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
65   70   75   80

Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
                85   90   95

Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
            100   105   110

Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val
        115   120   125

Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
    130   135   140

Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
145   150   155   160

Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
                165   170   175

His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
            180   185   190

Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
        195   200   205

Arg Ser Val Glu Gly Ser Cys Gly Phe
    210   215

<210> 49
<211> 963
<212> DNA
<213> Homo sapiens

<400> 49

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120

gtcccggccg agtgcttcga cctgctggtc cgccactgcg tggcctgcgg gctcctgcgc
180

acgccgcggc cgaaaccggc cggggccagc agccctgcgc caggacggc gctgcagccg
240

caggagtcgg tgggcgcggg ggccggcgag gcggcggtcg acaaaactca cacatgccca
300

ccgtgcccag cacctgaact cctggggggga ccgtcagtct tcctcttccc cccaaaaccc
360

aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtggtggt ggacgtgagc
420

cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc
480

aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc
540

gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc
600

ctcccagccc ccatcgagaa aaccatctcc aaagccaaag gcagccccg agaaccacag
660

gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc
720

ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg
780

gagaacaact acaagaccac gcctcccgtg ttggactccg acggctcctt cttcctctac
840

agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg
900

atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggaaa
960

tga
963

<210> 50
<211> 320
<212> PRT
<213> Homo sapiens

<400> 50
Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1   5   10   15

Gly Ser Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg

                    20   .25   ᴗ   ᴊ0

Asp Ala Pro Ala Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu
        35   40   45

Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro
    50   55   60

Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro
65   70   75   80

Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr
            85   90   95

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
        100   105   110

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
    115   ,   120   125

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
    130   135   140

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
145   150   155   160

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
            165   . 170   175

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
            180   185   190

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
            195   200   205

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
    210   215   220

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
225   230   235   240

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
            245   250   255

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
            260   265   270

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
            275   280   285

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
    290   295   300

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
305   310   315   320

<210>   51
<211>   107
<212>   PRT
<213>   Homo sapiens

<400> 51

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
                20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
            35   40   45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
            100   105

<210>   52
<211>   107
<212>   PRT
<213>   Mus musculus

<400>   52

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1   5   10   15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
                20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile
            35   40   45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65   70   75   80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
                85   90   95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105

<210>   53
<211>   119
<212>   PRT
<213>   Homo sapiens

<400>   53

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
            20   25   30

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Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
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Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
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Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
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Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
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Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
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Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
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Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
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Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
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Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
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Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
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Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
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Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
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Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
    50                  55                  60

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65                  70                  75                  80

Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
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Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
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Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
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Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
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Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
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His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
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Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg Val
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Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
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cctcaccgcg gcatcaagca ggtccggacc cactggctgc tggagcttgt caccaccagg
300

gggtccactg acggggcct gagctacaac ttcacccacc tggacgggta cttggacctt
360

ctcagggaga accagctcct cccagggttt gagctgatgg gcagcgcctc gggccacttc
420

actgactttg aggacaagca gcaggtgttt gagtggaagg acttggtctc cagcctggcc
480

aggagataca tcggtaggta cggactggcg catgtttcca gtggaactt cgagacgtgg
540

aatgagccag accaccacga ctttgacaac gtctccatga ccatgcaagg cttcctgaac
600

tactacgatg cctgctcgga gggtctgcgc gccgccagcc ccgccctgcg gctgggaggc
660

cccggcgact ccttccacac cccaccgcga tccccgctga ctggggcct cctgcgccac
720

tgccacgacg gtaccaactt cttcactggg gaggcgggcg tgcggctgga ctacatctcc
780

ctccacagga agggtgcgcg cagctccatc tccatcctgg agcaggagaa ggtcgtcgcg
840

cagcagatcc ggcagctctt ccccaagttc gcggacaccc ccatttacaa cgacgaggcg
900

gacccgctgg tgggctggtc cctgccacag ccgtggaggg cggacgtgac ctacgcggcc
960

atggtggtga aggtcatcgc gcagcatcag aacctgctac tggccaacac cacctccgcc
1020

ttcccctacg cgctcctgag caacgacaat gccttcctga ctaccacccc gcaccccttc
1080

gcgcagcgca cgctcaccgc gcgcttccag gtcaacaaca cccgcccgcc gcacgtgcag
1140

ctgttgcgca agccggtgct cacggccatg gggctgctgg cgctgctgga tgaggagcag
1200

ctctgggccg aagtgtcgca ggccgggacc gtcctggaca gcaaccacac ggtgggcgtc
1260

86

ctggccagcg cccaccgccc ccagggcccg gccgacgcct ggcgcgccgc ggtgctgatc
1320

tacgcgagcg acgacacccg cgcccacccc aaccgcagcg tcgcggtgac cctgcggctg
1380

cgcggggtgc cccccggccc gggcctggtc tacgtcacgc gctacctgga caacgggctc
1440

tgcagccccg acggcgagtg gcggcgcctg gccggcccg tcttccccac.ggcagagcag
1500

ttccggcgca tgcgcgcggc tgaggacccg gtggccgcgg cgccccgccc cttacccgcc
1560

ggcggccgcc tgaccctgcg ccccgcgctg cggctgccgt cgctttttgct ggtgcacgtg
1620

tgtgcgcgcc ccgagaagcc gcccgggcag gtcacgcggc tccgcgccct gcccctgacc
1680

caagggcagc tggttctggt ctggtcggat gaacacgtgg gctccaagtg cctgtggaca
1740

tacgagatcc agttctctca ggacggtaag gcgtacaccc cggtcagcag gaagccatcg
1800

accttcaacc tctttgtgtt cagcccagac acaggtgctg tctctggctc ctaccgagtt
1860

cgagccctgg actactgggc ccgaccaggc cccttctcgg accctgtgcc gtacctggag
1920

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1962

<210> 66
<211> 653
<212> PRT
<213> Homo sapiens

<400> 66
Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser
1   5   10   15

Leu Leu Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val
            20   25   30

Gln Val Asp Ala Ala Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg
        35   40   45

Ser Thr Gly Phe Cys Pro Pro Leu Pro His Ser Gln Ala Asp Gln Tyr
    50   55   60

Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala Tyr Val Gly Ala Val
65   70   75   80

Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu Glu Leu
                85   90   95

Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr

87

                  100   105   110

His Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro
         115   120   125

Gly Phe Glu Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu
         130   135   140

Asp Lys Gln Gln Val Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala
145   150   155   160

Arg Arg Tyr Ile Gly Arg Tyr Gly Leu Ala His Val Ser Lys Trp Asn
              165   170   175

Phe Glu Thr Trp Asn Glu Pro Asp His His Asp Phe Asp Asn Val Ser
              180   185   190

Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys Ser Glu Gly
         195   200   205

Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser
         210   215   220

Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His
225   230   235   240

Cys His Asp Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu
              245   250   255

Asp Tyr Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile
              260   265   270

Leu Glu Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro
         275   280   285

Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val
         290   295   300

Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala
305   310   315   320

Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn
              325   330   335

Thr Thr Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe
              340   345   350

Leu Ser Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg
              355   360   365

Phe Gln Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys
         370   375   380

Pro Val Leu Thr Ala Met Gly Leu Leu Ala Leu Leu Asp Glu Glu Gln
385   390   395   400

Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His
              405   410   415

Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala Asp
              420   425   430

88

```
Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala
        435             440             445

His Pro Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro
    450             455             460

Pro Gly Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu
465             470             475             480

Cys Ser Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro
            485             490             495

Thr Ala Glu Gln Phe Arg Arg Met Arg Ala Ala Glu Asp Pro Val Ala
        500             505             510

Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu Thr Leu Arg Pro
        515             520             525

Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro
    530             535             540

Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr
545             550             555             560

Gln Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys
            565             570             575

Cys Leu Trp Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr
        580             585             590

Thr Pro Val Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser
        595             600             605

Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr Arg Val Arg Ala Leu Asp
    610             615             620

Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu
625             630             635             640

Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro
            645             650
```

<210> 67
<211> 1290
<212> DNA
<213> Homo sapiens

<400> 67
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60

ctcgtttcct gggacatccc tggggctaga gcactggaca atggattggc aaggacgcct
120

accatgggct ggctgcactg ggagcgcttc atgtgcaacc ttgactgcca ggaagagcca
180

gattcctgca tcagtgagaa gctcttcatg gagatggcag agctcatggt ctcagaaggc
240

tggaaggatg caggttatga gtacctctgc attgatgact gttggatggc tccccaaaga
300

gattcagaag gcagacttca ggcagaccct cagcgctttc ctcatgggat cgccagcta
360

gctaattatg ttcacagcaa aggactgaag ctagggattt atgcagatgt tggaaataaa
420

acctgcgcag gcttccctgg gagttttgga tactacgaca ttgatgccca gacctttgct
480

gactggggag tagatctgct aaaatttgat ggttgttact gtgacagttt ggaaaatttg
540

gcagatggtt ataagcacat gtccttggcc ctgaatagga ctggcagaag cattgtgtac
600

tcctgtgagt ggcctcttta tatgtggccc tttcaaaagc ccaattatac agaaatccga
660

cagtactgca atcactggcg aaattttgct gacattgatg attcctggaa aagtataaag
720

agtatcttgg actggacatc ttttaaccag gagagaattg ttgatgttgc tggaccaggg
780

ggttggaatg acccagatat gttagtgatt ggcaactttg cctcagctg gaatcagcaa
840

gtaactcaga tggccctctg ggctatcatg gctgctcctt tattcatgtc taatgacctc
900

cgacacatca gccctcaagc caaagctctc cttcaggata aggacgtaat tgccatcaat
960

caggacccct tgggcaagca agggtaccag cttagacagg agacaacttt gaagtgtgg
1020

gaacgacctc tctcaggctt agcctgggct gtagctatga taaaccggca ggagattggt
1080

ggacctcgct cttataccat cgcagttgct tccctgggta aaggagtggc ctgtaatcct
1140

gcctgcttca tcacacagct cctccctgtg aaaaggaagc tagggttcta tgaatggact
1200

tcaaggttaa gaagtcacat aaatcccaca ggcactgttt tgcttcagct agaaaataca
1260

atgcagatgt cattaaaaga cttactttaa
1290

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<210>  68
<211>  429
<212>  PRT
<213>  Homo sapiens

<400>  68
Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu
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Arg Phe Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu
            20   25   30

Asp Asn Gly Leu Ala Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu
        35   40   45

Arg Phe Met Cys Asn Leu Asp Cys Gln Glu Glu Pro Asp Ser Cys Ile
    50   55   60

Ser Glu Lys Leu Phe Met Glu Met Ala Glu Leu Met Val Ser Glu Gly
65   70   75   80

Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp Cys Trp Met
                85   90   95

Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln Arg
            100   105   110

Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly
        115   120   125

Leu Lys Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly
    130   135   140

Phe Pro Gly Ser Phe Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala
145   150   155   160

Asp Trp Gly Val Asp Leu Leu Lys Phe Asp Gly Cys Tyr Cys Asp Ser
                165   170   175

Leu Glu Asn Leu Ala Asp Gly Tyr Lys His Met Ser Leu Ala Leu Asn
            180   185   190

Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro Leu Tyr Met
        195   200   205

Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn
    210   215   220

His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys
225   230   235   240

Ser Ile Leu Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val
                245   250   255

Ala Gly Pro Gly Gly Trp Asn Asp Pro Asp Met Leu Val Ile Gly Asn
            260   265   270

Phe Gly Leu Ser Trp Asn Gln Gln Val Thr Gln Met Ala Leu Trp Ala
        275   280   285

Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp Leu Arg His Ile Ser
    290   295   300

Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala Ile Asn
305   310   315   320

Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn
                325   330   335

Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala
            340   345   350

Met Ile Asn Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala
            355   360   365

Val Ala Ser Leu Gly Lys Gly Val Ala Cys Asn Pro Ala Cys Phe Ile
    370   375   380

Thr Gln Leu Leu Pro Val Lys Arg Lys Leu Gly Phe Tyr Glu Trp Thr
385   390   395   400

Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr Val Leu Leu Gln
            405   410   415

Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu
            420   425

<210>   69
<211>   351
<212>   DNA
<213>   Homo sapiens

<400>   69
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60

gttctccatt ccgctcctga tgtgcaggat tgcccagaat gcacgctaca ggaaaaccca
120

ttcttctccc agccgggtgc cccaatactt cagtgcatgg gctgctgctt ctctagagca
180

tatcccactc cactaaggtc caagaagacg atgttggtcc aaaagaacgt cacctcagag
240

tccacttgct gtgtagctaa atcatataac agggtcacag taatggggggg tttcaaagtg
300

gagaaccaca cggcgtgcca ctgcagtact tgttattatc acaaatctta a
351

<210>   70
<211>   116
<212>   PRT
<213>   Homo sapiens

<400>   70
Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
1   5   10   15

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
            20   25   30

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
            35   40   45

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
    50   55   60

```
Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65                  70              75                  80

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
                85              90                  95

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
            100             105             110

Tyr His Lys Ser
        115
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<210> 71
<211> 498
<212> DNA
<213> Homo sapiens

<400> 71
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60

tccaaggagc cgcttcggcc acggtgccgc cccatcaatg ccaccctggc tgtggagaag
120

gagggctgcc ccgtgtgcat caccgtcaac accaccatct gtgccggcta ctgccccacc
180

atgacccgcg tgctgcaggg ggtcctgccg gccctgcctc aggtggtgtg caactaccgc
240

gatgtgcgct tcgagtccat ccggctccct ggctgcccgc gcggcgtgaa ccccgtggtc
300

tcctacgccg tggctctcag ctgtcaatgt gcactctgcc gccgcagcac cactgactgc
360

gggggtccca aggaccaccc cttgacctgt gatgaccccc gcttccagga ctcctcttcc
420

tcaaaggccc ctccccccag ccttccaagc ccatcccgac tcccggggcc ctcggacacc
480

ccgatcctcc cacaataa
498
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<210> 72
<211> 165
<212> PRT
<213> Homo sapiens

<400> 72
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Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly
1               5               10                  15

Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile
            20              25              30

Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr
        35              40              45

Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val
```

                          50   55   60

Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg
65   70   75   80

Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val
                85   90   95

Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu
            100   105   110

Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu
            115   120   125

Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro
    130   135   140

Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
145   150   155   160

Pro Ile Leu Pro Gln
                165

<210> 73
<211> 165
<212> PRT
<213> Homo sapiens

<400> 73
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
 1   5   10   15

Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
            20   25   30

Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
        35   40   45

Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
    50   55   60

Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
65   70   75   80

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
                85   90   95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
            100   105   110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
            115   120   125

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
    130   135   140

Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
145   150   155   160

Cys Arg Thr Gly Asp
                165

<210> 74
<211> 588
<212> DNA
<213> Homo sapiens

<400> 74
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60

tctctgggct gtgatctgcc tcagaaccat ggcctactta gcaggaacac cttggtgctt
120

ctgcaccaaa tgaggagaat ctccccttttc ttgtgtctca aggacagaag agacttcagg
180

ttcccccagg agatggtaaa agggagccag ttgcagaagg cccatgtcat gtctgtcctc
240

catgagatgc tgcagcagat cttcagcctc ttccacacag agcgctcctc tgctgcctgg
300

aacatgaccc tcctagacca actccacact ggacttcatc agcaactgca acacctggag
360

acctgcttgc tgcaggtagt gggagaagga gaatctgctg gggcaattag cagccctgca
420

ctgaccttga ggaggtactt ccagggaatc cgtgtctacc tgaaagagaa gaaatacagc
480

gactgtgcct gggaagttgt cagaatggaa atcatgaaat ccttgttctt atcaacaaac
540

atgcaagaaa gactgagaag taaagataga gacctgggct catcttga
588

<210> 75
<211> 195
<212> PRT
<213> Homo sapiens

<400> 75
Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
1   5   10   15

Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
            20   25   30

Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
        35   40   45

Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
    50   55   60

Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
65   70   75   80

His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
                85   90   95

Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu
            100   105   . 110

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
        115   120   125

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg
    130   135   140

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser
145   150   155   160

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe
            165   170   175

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu
            180   185   190

Gly Ser Ser
        195

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